

SEQUENCE ID LISTING

SEQ ID NO: 1 is the amino acid sequence of residues 33-79 of c-Jun.

SEQ ID NO: 2 is the nucleotide sequence for an N-terminal primer used for producing c-Jun truncation mutants.

- 5 SEQ ID NO: 3 is the nucleotide sequence for an N-terminal primer used for producing c-Jun truncation mutants.

SEQ ID NO: 4 is the nucleotide sequence for an N-terminal primer used for producing c-Jun truncation mutants.

- 10 SEQ ID NO: 5 is the nucleotide sequence for an N-terminal primer used for producing c-Jun truncation mutants.

SEQ ID NO: 6 is the nucleotide sequence for an N-terminal primer used for producing c-Jun truncation mutants.

SEQ ID NO: 7 is the nucleotide sequence for a C-terminal primer used for producing c-Jun truncation mutants.

- 15 SEQ ID NO: 8 is the nucleotide sequence for a C-terminal primer used for producing c-Jun truncation mutants.

SEQ ID NO: 9 is the nucleotide sequence and deduced amino acid sequence for *c-jun* and c-Jun.

SEQ ID NO: 10 is the deduced amino acid sequence of c-Jun.

08799913-021397
465720-ET665280

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS: Karin, Michael
Hibi, Masahiko
Lin, Anning

(ii) TITLE OF INVENTION: ONCOPROTEIN PROTEIN KINASE

(iii) NUMBER OF SEQUENCES: 10

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Spensley Horn Jubas & Lubitz
(B) STREET: 1880 Century Park East, Suite 500
(C) CITY: Los Angeles
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 90067

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US
(B) FILING DATE: 18 JUL-1994
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Wetherell, Jr., Ph.D., John R.,
(B) REGISTRATION NUMBER: 31,678
(C) REFERENCE/DOCKET NUMBER: PD-3701

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (619) 455-5100
(B) TELEFAX: (619) 455-5110

1994-07-20 14:39:20

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (B) CLONE: c-Jun/JNK binding site

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..47

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ile	Leu	Lys	Gln	Ser	Met	Thr	Leu	Asn	Leu	Ala	Asp	Pro	Val	Gly	Ser
1				5					10					15	
Leu	Lys	Pro	His	Leu	Arg	Ala	Lys	Asn	Ser	Asp	Leu	Leu	Thr	Ser	Pro
			20					25					30		
Asp	Val	Gly	Leu	Leu	Lys	Leu	Ala	Ser	Pro	Glu	Leu	Glu	Arg	Leu	
		35					40					45			

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: N-terminal primer

08799913.021397

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

5 TCTGCAGGAT CCCCATGACT GCAAAGATGG AAACG

35

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: N-terminal primer

15

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..34

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TCTGCAGGAT CCCCGACGAT GCCCTCAACG CCTC

34

20

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: N-terminal primer

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(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

5 TCTGCAGGAT CCCCAGAGAGC GGACCTTATG GCTAC

35

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: N-terminal primer

15

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TCTGCAGGAT CCCCAGGAC CCAGTGGGGA GCCTG

35

20

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: N-terminal primer

26ET20"ET66480

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

5 TCTGCAGGAT CCCCAAGAAC TCGGACCTCC TCACC

35

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: C-terminal primer

15 (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TGAATTCCTGC AGGCGCTCCA GCTCGGGCGA

30

20 (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: C-terminal primer

2669913-01397

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..33

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

5 TGAATTCCTG CAGGTCGGCG TGGTGGTGAT GTG

33

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2096 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

(B) CLONE: Jun

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 412..1404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAATTCGGGG GCGGCCAAGA CCCGCCGCCG GCCGGCCACT GCAGGGTCCG CACTGATCCG 60

20 CTCCGGCGGA GAGCCGCTGC TCTGGAAGT CAGTTCGCCT GCGGACTCCG AGGAACCGCT 120

GCGCACGAAG AGCCGTCAGT GAGTGACCGC GACTTTTCAA AGCCGGGTAG GGCGCGCGAG 180

TCGACAAGTA AGAGTGCGGG AGGCATCTTA ATTAACCCTG CGCTCCCTGG AGCAGCTGGT 240

GAGGAGGGCG CACGGGGACG ACAGCCAGCG GGTGCGTGCG CTCTTAGAGA AACTTTCCCT 300

GTCAAAGGCT CCGGGGGGCG CGGGTGTCCC CCGCTTGCCA CAGCCCTGTT GCGGCCCCGA 360

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	AACTTGTGCG CGCAGCGCAA ACTAACCTCA CGTGAAGTGA CGGACTGTC T ATC ACT	417
	Met Thr 1	
5	GCA AAG ATG GAA ACG ACC TTC TAT GAC GAT GCC CTC AAC GCC TCG TTC Ala Lys Met Glu Thr Thr Phe Tyr Asp Asp Ala Leu Asn Ala Ser Phe 5 10 15	465
	CTC CCC TCC GAG AGG GGA CCT TAT GGC TAC AGT AAC CCC AAG ATC CTG Leu Pro Ser Glu Arg Gly Pro Tyr Gly Tyr Ser Asn Pro Lys Ile Leu 20 25 30	513
10	AAA CAG AGC ATG ACC CTG AAC CTG GCC GAC CCA GTG GGG AGC CTG AAG Lys Gln Ser Met Thr Leu Asn Leu Ala Asp Pro Val Gly Ser Leu Lys 35 40 45 50	561
15	CCG CAC CTC CGC GCC AAG AAC TCG GAC CTC CTC ACC TCG CCC GAC GTG Pro His Leu Arg Ala Lys Asn Ser Asp Leu Leu Thr Ser Pro Asp Val 55 60 65	609
	GGG CTG CTC AAG CTG GCG TCG CCC GAG CTG GAG CGC CTG ATA ATC CAG Gly Leu Leu Lys Leu Ala Ser Pro Glu Leu Glu Arg Leu Ile Ile Gln 70 75 80	657
20	TCC AGC AAC GGG CAC ATC ACC ACC ACG CCG ACC CCC ACC CAG TTC CTG Ser Ser Asn Gly His Ile Thr Thr Thr Pro Thr Pro Thr Gln Phe Leu 85 90 95	705
	TGC CCC AAG AAC GTG ACA GAT GAG CAG GAG GGG TTC GCC GAG GGC TTC Cys Pro Lys Asn Val Thr Asp Glu Gln Glu Gly Phe Ala Glu Gly Phe 100 105 110	753
25	GTG CGC GCC CTG GCC GAA CTG CAC AGC CAG AAC ACG CTG CCC AGC GTC Val Arg Ala Leu Ala Glu Leu His Ser Gln Asn Thr Leu Pro Ser Val 115 120 125 130	801
30	ACG TCG GCG GCG CAG CCG GTC AAC GGG GCA GGC ATG GTG GCT CCC GCG Thr Ser Ala Ala Gln Pro Val Asn Gly Ala Gly Met Val Ala Pro Ala 135 140 145	849
	GTA GCC TCG GTG GCA GGG GGC AGC GGC AGC GGC GGC TTC AGC GCC AGC Val Ala Ser Val Ala Gly Gly Ser Gly Ser Gly Gly Phe Ser Ala Ser 150 155 160	897
	CTG CAC AGC GAG CCG CCG GTC TAC GCA AAC CTC AGC AAC TTC AAC CCA	945

26ET20-ET56480

	Leu	His	Ser	Glu	Pro	Pro	Val	Tyr	Ala	Asn	Leu	Ser	Asn	Phe	Asn	Pro	
				165				170					175				
5	GGC	GCG	CTG	AGC	AGC	GGC	GGC	GGG	GCG	CCC	TCC	TAC	GGG	GCG	GCC	GGC	993
	Gly	Ala	Leu	Ser	Ser	Gly	Gly	Gly	Ala	Pro	Ser	Tyr	Gly	Ala	Ala	Gly	
		180					185				190						
	CTG	GCC	TTT	CCC	GCG	CAA	CCC	CAG	CAG	CAG	CAG	CAG	CCG	CCG	CAC	CAC	1041
	Leu	Ala	Phe	Pro	Ala	Gln	Pro	Gln	Gln	Gln	Gln	Gln	Pro	Pro	His	His	
	195					200				205						210	
10	CTG	CCC	CAG	CAG	ATG	CCC	GTG	CAG	CAC	CCG	CGG	CTG	CAG	GCC	CTG	AAG	1089
	Leu	Pro	Gln	Gln	Met	Pro	Val	Gln	His	Pro	Arg	Leu	Gln	Ala	Leu	Lys	
					215					220					225		
	GAG	GAG	CCT	CAG	ATA	GTG	CCC	GAG	ATG	CCC	GGC	GAG	ACA	CCG	CCC	CTG	1137
	Glu	Glu	Pro	Gln	Ile	Val	Pro	Glu	Met	Pro	Gly	Glu	Thr	Pro	Pro	Leu	
				230					235					240			
15	TCC	CCC	ATC	GAC	ATG	GAG	TCC	CAG	GAG	CGC	ATC	AAG	GCG	GAG	AGG	AAG	1185
	Ser	Pro	Ile	Asp	Met	Glu	Ser	Gln	Glu	Arg	Ile	Lys	Ala	Glu	Arg	Lys	
			245					250				255					
	CGC	ATG	AGG	AAC	CGC	ATC	GCT	GCC	TGG	AAG	TGC	CGA	AAA	AGG	AAG	CTG	1233
	Arg	Met	Arg	Asn	Arg	Ile	Ala	Ala	Ser	Lys	Cys	Arg	Lys	Arg	Lys	Leu	
20		260				265					270						
	GAG	AGA	ATC	GCC	CGG	CTG	GAG	GAA	AAA	GTG	AAA	ACC	TTG	AAA	GCT	CAG	1281
	Glu	Arg	Ile	Ala	Arg	Leu	Glu	Glu	Lys	Val	Lys	Thr	Leu	Lys	Ala	Gln	
	275					280				285						290	
25	AAC	TCG	GAG	CTG	GCG	TCG	ACG	GCC	AAC	ATG	CTC	AGG	GAA	CAG	GTC	GCA	1329
	Asn	Ser	Glu	Leu	Ala	Ser	Thr	Ala	Asn	Met	Leu	Arg	Glu	Gln	Val	Ala	
					295					300					305		
	CAG	CTT	AAA	CAC	AAA	GTC	ATG	AAC	CAC	GTT	AAC	AGT	GGG	TGC	CAA	CTC	1377
	Gln	Leu	Lys	His	Lys	Val	Met	Asn	His	Val	Asn	Ser	Gly	Cys	Gln	Leu	
				310					315					320			
30	ATC	CTA	ACG	CAG	CAG	TTG	CAA	ACA	TTT	TGAAGAGAGA	CCGTCGGGGG						1424
	Ile	Leu	Thr	Gln	Gln	Leu	Gln	Thr	Phe								
			325					330									
	CTGAGGGGCA	ACGAAGAAAA	AAAATAACAC	AGAGAGACAG	ACTTGAGAAC	TTGACAAGTT											1484

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CCGACGGAGA GAAAAAAGAA GTGTCCGAGA ACTAAAGCCA AGGGTATCCA AGTTGGACTG 1544
GGTTCGGTCT GACGGCGCCC CCAGTGTGCA CGAGTGGGAA CCACCTGGTC GCGCCCTCCC 1604
TTGGCGTCGA GCCAGGGAGC GGCCGCCTGG GGGCTGCCCC GCTTTCGGGA CGGGCTGTCC 1664
CCGCGCGAAC GGAACGTTGG ACTTTCGTTA ACATTGACCA AGAACTGCAT GGACCTAACA 1724
5 TTCGATCTCA TTCAGTATTA AAGGGGGCAG GGGGAGGGGG TTACAAACTG CAATAGAGAC 1784
TGTAGATTGC TTCTGTAGTA CTCCTTAAGA ACACAAAGCG GGGGGAGGGT TGGGGAGGGG 1844
CGGCAGGAGG GAGGTTTGTG AGAGCGAGGC TGAGCCTACA GATGAACTCT TTCTGGCCTG 1904
CTTTCGTAA CTGTGTATGT ACATATATAT ATTTTAAAT TTGATTAAAG CTGATTACTG 1964
TCAATAAACA GCTTCATGCC TTGTAAAGTT ATTTCTTGTG TGTGTTTGG GGATCCTGCC 2024
10 CAGTGTGTGTT TGTAATAAAG AGATTGGAG CACTCTGAGT TTACCATTG TAATAAAGTA 2084
TATAATTTTT TT 2096

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

20 Met Thr Ala Lys Met Glu Thr Thr Phe Tyr Asp Asp Ala Leu Asn Ala
1 5 10 15
Ser Phe Leu Pro Ser Glu Arg Gly Pro Tyr Gly Tyr Ser Asn Pro Lys
20 25 30
Ile Leu Lys Gln Ser Met Thr Leu Asn Leu Ala Asp Pro Val Gly Ser
35 40 45
25 Leu Lys Pro His Leu Arg Ala Lys Asn Ser Asp Leu Leu Thr Ser Pro
50 55 60

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Asp Val Gly Leu Leu Lys Leu Ala Ser Pro Glu Leu Glu Arg Leu Ile
 65 70 75 80
 Ile Gln Ser Ser Asn Gly His Ile Thr Thr Thr Pro Thr Pro Thr Gln
 85 90 95
 5 Phe Leu Cys Pro Lys Asn Val Thr Asp Glu Gln Glu Gly Phe Ala Glu
 100 105 110
 Gly Phe Val Arg Ala Leu Ala Glu Leu His Ser Gln Asn Thr Leu Pro
 115 120 125
 10 Ser Val Thr Ser Ala Ala Gln Pro Val Asn Gly Ala Gly Met Val Ala
 130 135 140
 Pro Ala Val Ala Ser Val Ala Gly Gly Ser Gly Ser Gly Gly Phe Ser
 145 150 155 160
 Ala Ser Leu His Ser Glu Pro Pro Val Tyr Ala Asn Leu Ser Asn Phe
 165 170 175
 15 Asn Pro Gly Ala Leu Ser Ser Gly Gly Gly Ala Pro Ser Tyr Gly Ala
 180 185 190
 Ala Gly Leu Ala Phe Pro Ala Gln Pro Gln Gln Gln Gln Gln Pro Pro
 195 200 205
 20 His His Leu Pro Gln Gln Met Pro Val Gln His Pro Arg Leu Gln Ala
 210 215 220
 Leu Lys Glu Glu Pro Gln Ile Val Pro Glu Met Pro Gly Glu Thr Pro
 225 230 235 240
 Pro Leu Ser Pro Ile Asp Met Glu Ser Gln Glu Arg Ile Lys Ala Glu
 245 250 255
 25 Arg Lys Arg Met Arg Asn Arg Ile Ala Ala Ser Lys Cys Arg Lys Arg
 260 265 270
 Lys Leu Glu Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu Lys
 275 280 285
 30 Ala Gln Asn Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu Gln
 290 295 300

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Val Ala Gln Leu Lys His Lys Val Met Asn His Val Asn Ser Gly Cys
305 310 315 320

Gln Leu Ile Leu Thr Gln Gln Leu Gln Thr Phe
325 330

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